

DATE: 02/08/2002 RAW SEQUENCE LISTING TIME: 07:35:25 PATENT APPLICATION: US/09/816,653A

Input Set : A:\09-816,653 corrected seq. list. 10716.57.txt

Output Set: N:\CRF3\02082002\I816653A.raw

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3 <110> APPLICANT: Rastelli, Luca
             Pennica, Diane
     6 <120> TITLE OF INVENTION: NOVEL HUMAN STRA6-LIKE PROTEIN AND NUCLEIC ACIDS ENCODING
THE SAME
     8 <130> FILE REFERENCE: 10716/57
    10 <140> CURRENT APPLICATION NUMBER: 09/816,653A
    11 <141> CURRENT FILING DATE: 2001-03-23
                                                                   ENTERED
    13 <150> PRIOR APPLICATION NUMBER: 60/191,532
    14 <151> PRIOR FILING DATE: 2000-03-23
     16 <160> NUMBER OF SEQ ID NOS: 7
    18 <170> SOFTWARE: PatentIn version 3.1
    20 <210> SEQ ID NO: 1
    21 <211> LENGTH: 598
     22 <212> TYPE: DNA
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26 <221> NAME/KEY: misc_feature

27 <222> LOCATION: (92)..(92)

28 <223> OTHER INFORMATION: n is a, t, c or g

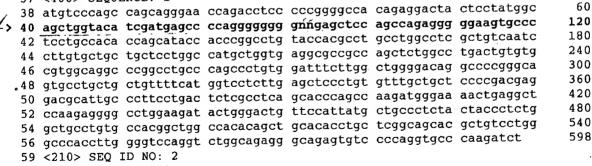
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34 <223> OTHER INFORMATION: n is a, t, c or g

37 <400> SEQUENCE: 1



60 <211> LENGTH: 199

61 <212> TYPE: PRT

62 <213> ORGANISM: Homo sapiens hSTRA6 amino terminal polypeptide fragment

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66 <222> LOCATION: (31)..(31)

67 <223> OTHER INFORMATION: Xaa is any amino acid

70 <400> SEQUENCE: 2

72 Met Ser Gln Pro Ala Gly Asn Gln Thr Ser Pro Gly Ala Thr Glu Asp

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76 Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gln Gly Gly Xaa Glu 25 20 80 Leu Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile Pro Pro 40 84 Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val Leu Leu 88 Leu Leu Ala Met Leu Val Arg Arg Gln Leu Trp Pro Asp Cys Val 70 75 92 Arg Gly Arg Pro Gly Leu Pro Ser Pro Val Asp Phe Leu Ala Gly Asp 90 85 96 Arg Pro Arg Ala Val Pro Ala Ala Val Phe Met Val Leu Leu Ser Ser 105 110 100 100 Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala Leu Pro Phe Leu Thr Leu 120 115 101 104 Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr Glu Ala Pro Arg Gly Ala 135 108 Trp Lys Ile Leu Gly Leu Phe His Tyr Ala Ala Leu Tyr Tyr Pro Leu 150 109 145 112 Ala Ala Cys Ala Thr Ala Gly His Thr Ala Ala His Leu Leu Gly Ser 170 165 116 Thr Leu Ser Trp Ala His Leu Gly Val Gln Val Trp Gln Arg Ala Glu 185 117 180 120 Cys Pro Gln Val Pro Lys Ile 121 195 124 <210> SEQ ID NO: 3 125 <211> LENGTH: 1351 126 <212> TYPE: DNA 127 <213> ORGANISM: Homo sapiens hSTRA6 nucleotide fragment, 3' region 129 <220> FEATURE: 130 <221> NAME/KEY: misc_feature 131 <222> LOCATION: (437)...(437) 132 <223> OTHER INFORMATION: n is a, t, c or g 135 <220> FEATURE: 136 <221> NAME/KEY: misc_feature 137 <222> LOCATION: (438)..(438) 138 <223> OTHER INFORMATION: n is a, t, c or g 141 <220> FEATURE: 142 <221> NAME/KEY: misc_feature 143 <222> LOCATION: (439)..(439) 144 <223> OTHER INFORMATION: n is a, t, c or g 147 <220> FEATURE: 148 <221> NAME/KEY: misc_feature 149 <222> LOCATION: (440)..(440) 150 <223> OTHER INFORMATION: n is a, t, c or g 153 <220> FEATURE: 154 <221> NAME/KEY: misc_feature 155 <222> LOCATION: (441)..(441)

156 <223> OTHER INFORMATION: n is a, t, c or g

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179 <222> LOCATION: (874)..(874)
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209 <222> LOCATION: (1174) .. (1174)
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222 <223> OTHER INFORMATION: n is a, t, c or q
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226 <221> NAME/KEY: misc_feature
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228 <223> OTHER INFORMATION: n is a, t, c or g
231 <400> SEOUENCE: 3
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232 tyctacatct cagcettggt ettgteetge ttacteacet teetggteet gatgegetea
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  234 ctgqtqacac acaggcttgg ttctgggggc agcggggatg gccagttttc atggaacctg
                                                                            120
  236 ttttctgtcc ccctgccact cccgcccctg gcagggctcc tggtgcagca gatcatcttc
  238 ttcctqqqaa ccacqqccct ggccttcctg gtgctcatgc ctgtgctcca tggcaggaac
                                                                            240
  240 etcetgttet teegtteeet ggagteeteg tggeeettet ggetgaettt ggeeetgget
                                                                            300
  242 qtqatcctqc agaacatgqc agcccattqq qtcttcctqq agactcatqa tqqacaccca
                                                                            420
  244 cagctgacca accggcgagt gctctatgca gccacctttc ttctcttccc cctcaatgtg
 246 ctggtgggtg ccatggnnnn noctgctcc cccagcattg ccatccgcca ccccaccca
                                                                            480
  248 ggctactaca cgtaccgaaa cttcttgaag attgaagtca gccagtcgca tccagccatg
                                                                            540
  250 acageettet geteeetget eetgeaageg cagageetee tacceaggae catggeagee
                                                                            600
  252 ccccaqqaca gcctcaqacc aggggaggaa gacgaaggat gcagctgcta cagacaaagg
                                                                            660
> 254 actocatggc caagggaget aggcccgggg ccancegegg cagggetege tggggtetgg
                                                                            720
  256 cctacacget getgeacaac ccaaccetge aggtetteeg caagacggee etgttgggtg
                                                                            780
                                                                            840
  258 ccaatggtgc ccagccctgc tectecetec ceggetetec teccagcate acaccagcea
                                                                            900
260 tgcagccage aggteeteeg gateaengtg gttnggtgga ggtetgtetg caetgggage
> 262 ctcangangg ctctgctcca cccacttggc tatgggagag ccagcagggg ttctggagaa
  264 aaaaactggt gggttagggc cttggtccag gagccagttg agccagggca gccacatcca
                                                                           1020
  266 ggcgtctccc taccctggct ctgccatcag ccttgaaggg cctcgatgaa gccttctctg
                                                                           1080
  268 gaaccactee ageceágete caceteagee ttggeettea egetgtggaa geagecaagg
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>/270 cacttectea eccenteage gecaeggace thintgggga gtggceggaa agetecengg
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272 cctntggcct gcagggcagc ccaagtcatg_actcagacca_ggtcccacac_tgagctgccc___1260
> 274 acactcgaga gccagatatt tttgtagttt ttatnccttt ggctattatg aaagaggtta
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  276 gtgtgttccc tgcaataaac ttgttcctga g
                                                                           1351
  279 <210> SEQ ID NO: 4
  280 <211> LENGTH: 325
  281 <212> TYPE: PRT
  282 <213> ORGANISM: Homo sapiens hSTRA6 polypeptide fragment, carboxy terminus
  284 <220> FEATURE:
  285 <221> NAME/KEY: MISC_FEATURE
  286 <222> LOCATION: (146)..(148)
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   317 <223> OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
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   326 Leu Met Arg Ser Leu Val Thr His Arg Leu Gly Ser Gly Gly Ser Gly
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                                        25
   330 Asp Gly Gln Phe Ser Trp Asn Leu Phe Ser Val Pro Leu Pro Leu Pro
                                    40
   334 Pro Leu Ala Gly Leu Leu Val Gln Gln Ile Ile Phe Phe Leu Gly Thr
                               . 55
   338 Thr Ala Leu Ala Phe Leu Val Leu Met Pro Val Leu His Gly Arg Asn
                           70
                                                75
   342 Leu Leu Phe Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe Trp Leu Thr
                                            90
   346 Leu Ala Leu Ala Val Ile Leu Gln Asn Met Ala Ala His Trp Val Phe
                                        105
   347
   350 Leu Glu Thr His Asp Gly His Pro Gln Leu Thr Asn Arg Arg Val Leu
   351
               115
   354 Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu Val Gly Ala
                                135
           130
> 358 Met Xaa Xaa Kaa Cys Ser Pro Ser Ile Ala Ile Arg His Pro Thr Pro
                           150
   362 Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys Ile Glu Val Ser Gln Ser
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                                            170
   366 His Pro Ala Met Thr Ala Phe Cys Ser Leu Leu Gln Ala Gln Ser
                                        185
                   180
   370 Leu Leu Pro Arg Thr Met Ala Ala Pro Gln Asp Ser Leu Arg Pro Gly
                                    200
   374 Glu Glu Asp Glu Gly Met Gln Leu Leu Gln Thr Lys Asp Ser Met Ala
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                               215 .
   378 Lys Gly Ala Arg Pro Gly Ala Xaa Arg Gly Arg Ala Arg Trp Gly Leu
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   379 225
   382 Ala Tyr Thr Leu Leu His Asn Pro Thr Leu Gln Val Phe Arg Lys Thr
                       245
                                            250
   386 Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro Cys Ser Ser Leu Pro Gly
                                        265
                   260
   390 Ser Pro Pro Ser Ile Thr Pro Ala Met Gln Pro Ala Gly Pro Pro Asp
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            ~ 275
                                    280
                                                        285
 > 394 His Xaa Gly Xaa Val Glu Val Cys Leu His Trp Glu Pro Xaa Xaa Gly
   395
                               295
           290
   398 Ser Ala Pro Pro Thr Trp Leu Trp Glu Ser Gln Gln Gly Phe Trp Arg
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                                                315
                                                                     320
   402 Lys Lys Leu Val Gly
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   406 <210> SEQ ID NO: 5
   407 <211> LENGTH: 6964
   408 <212> TYPE: DNA
   409 <213> ORGANISM: Homo sapiens clone RP11-60L3, Sequencing in Progress, 9 unordered
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Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

pieces; GenBank AC023300, nts 150524 to 157487

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/816,653A

DATE: 02/08/2002

TIME: 07:35:26

Input Set : A:\09-816,653 corrected seq. list. 10716.57.txt

Output Set: N:\CRF3\02082002\1816653A.raw

L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4